aerosol, and is of questionable efficacy (McIntosh, 1990; Levin, 1994). Thus it is apparent that a greater understanding of the infectious mechanism and immunobiology of RSV is required to develop control measures based on vaccines or antiviral agents.

RSV belongs to the *Pneumovirus* genus of the Paramyxoviridae family of single strand negative sense RNA viruses, which includes other serious pathogens such as parainfluenza, mumps and measles (McIntosh, 1990; Kingsbury, 1990) and the recently identified zoonotic, equine morbillivirus (Murray *et al*, 1995). Like other Paramyxoviridase, RSV has two membrane glycoproteins which mediate invasion of susceptible cells (Morrison and Portner, 1991). One protein, the large glycoprotein or G protein, functions in attachment to cells. The other, the so-called fusion or F protein, causes fusion between the lipid of the viral membrane envelope and the cell plasma membrane lipid bilayer. RSV infection can also be transmitted by fusion of membranes of infected cells, which have F protein expressed on their surface, with adjacent cells.

The molecular architecture of the F protein is conserved between all members of the three genera of the Paramyxoviridae; however, each genus has a characteristic attachment protein (Morrison and Portner, 1991). Members of the *Paramyxovirus* genus have attachment proteins with neuraminidase and haemagglutinating activities; the attachment proteins of the *Morbillivirus* genus are haemagglutinins, but lack neuraminidase activity; and the attachment proteins of Pneumoviruses lack both haemagglutination and neuraminidase properties. Attachment proteins of the *Paramyxovirus* (Morrison and Portner, 1991) genus participate in sialic acid receptor-type interactions, which account for their ability to agglutinate red blood cells. RSV is also reported to interact with sialic acid; however, the mechanism of RSV G protein attachment and the identity of the cellular

for 1-1.5 hr at 0°C. Virus (50 µl) was then added and incubation continued for 1 hr at 0°C, followed by 4 days at 37°C without removal of excess peptide derivatives or virus. Monolayers were then fixed with formalin and stained with neutral red. Inhibition of cpe was determined by comparison with control cells infected with virus in the absence of any pepdtide derivatives. Monolayers were then fixed with formalin and viable cells stained with neutral red.

The binding of fluoresceinyl-149-197 and fluoresceinyl-163-197 to HEp-2 cells, demonstrated by flow cytometry and by confocal microscopy in the form of patches on the plasma membrane, shows that specific ligand binding interaction site(s) for cellular receptor(s) are contained within this region of the RSV G protein.

Peptide derivatives 1-4 (Figure 12) inhibited the cytopathic effect (cpe) of the A2 strain of human RSV on HEp-2 cells to different extents. The IC50 values for Ac149-177 and Ac149-190 were approximately 5-10 µM, which were comparatively more effective than the other peptide derivatives, which had IC50 values of approximately 50 µM. Oxidised A and B chains of insulin failed to inhibit the cpe of RSV on HEp-2 cells at 28 an 40 µM, respectively. Oxidised A and B chains of insulin failed to inhibit RSV-induced cpe of HEp-2 cells when included in these assays at 28 and 40 µM, respectively.

DISCUSSION

We have now shown that the disulphide bonding pattern of the ectodomain of the unusual attachment protein or G protein of RSV involves a preferred stable configuration with Cys173 linked to Cys186, and Cys176 linked to Cys182. This was achieved by a combination of analysis of proteolytic fragments of the protein and further analysis of metastable ions produced from the proteolytic fragments during MALDI-TOF-MS. These findings represent a potent demonstration of the utility of